AMENDMENTS TO THE CLAIMS

1. (currently amended) A genetic testing method for systemic lupus erythematosus (SLE) in a human subject, comprising:

a) collecting a tissue sample from a human subject;

b) amplifying nucleic acids from said tissue sample to obtain amplification products, said nucleic acids comprising a genomic sequence of human chromosome 1 between microsatellite markers D1S2860 and D1S213; and

c) detecting in the amplification products the presence or absence of a twelve-fold CA dinucleotide repeat consisting of (SEQ. ID. NO.:6), ~~wherein said CA dinucleotide repeat sequence is located in the genomic sequence upstream from a *PARP* transcription start site, corresponding to nucleotide positions 846 through 869 of (SEQ. ID. NO.:5), and~~ wherein the presence of said twelve-fold CA dinucleotide repeat ~~sequence~~ is diagnostic of SLE in a subject having SLE symptoms or indicates a genetic predisposition to develop SLE in a subject not presenting SLE symptoms.

2. (currently amended) The method of Claim 1, further comprising:

detecting in the amplification products the presence or absence of an eighteen-fold CA dinucleotide repeat consisting of (SEQ. ID. NO.:7), ~~wherein said eighteen-fold CA dinucleotide repeat sequence is located in the genomic sequence upstream from a *PARP* transcription start site, between nucleotide positions 845 and 869 of (SEQ. ID. NO.:5), and~~ wherein the absence of said eighteen-fold CA dinucleotide repeat ~~sequence~~ is diagnostic of SLE in subject having SLE symptoms or indicates a genetic predisposition to develop SLE in a subject not presenting SLE symptoms.

3. (original) The method of Claim 1, wherein the tissue sample is a blood sample.

4. (original) The method of Claim 1, wherein an oligonucleotide primer is used in amplifying said nucleic acids.

5. (original) The method of Claim 4, wherein said primer has a nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, or AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long.

6. (original) The method of Claim 4, wherein an oligonucleotide primer comprising nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.

7. (original) The method of Claim 4, wherein an oligonucleotide primer comprising nucleotide sequence AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.

8. (original) The method of Claim 4, wherein said oligonucleotide primer is labeled with a fluorescent dye.

9. (original) The method of Claim 8, wherein said dye is SYBR Green I, YO-PRO-1, thiazole orange, Hex, FAM or TET.

10-11. (canceled)

12. (currently amended) A genetic testing method for systemic lupus erythematosus (SLE) in a human subject, comprising:

a) collecting a tissue sample from a human subject;

b) amplifying nucleic acids from said tissue sample to obtain amplification products, said nucleic acids comprising a genomic sequence of human chromosome 1 between microsatellite markers D1S2860 and D1S213; and

c) detecting in the amplification products the presence or absence of an eighteen-fold CA dinucleotide repeat sequence consisting of (SEQ. ID. NO.:7), ~~wherein said eighteen-fold CA dinucleotide repeat sequence is located in the genomic sequence upstream from a *PARP* transcription start site, between nucleotide positions 845 and 869 of (SEQ. ID. NO.:5), and~~ wherein the absence of said eighteen-fold CA dinucleotide repeat ~~sequence~~ is diagnostic of SLE in a subject having SLE symptoms or indicates a genetic predisposition to develop SLE in a subject not presenting SLE symptoms.

13. (original) The method of Claim 12, wherein the tissue sample is a blood sample.

14. (original) The method of Claim 12, wherein an oligonucleotide primer is used in amplifying said nucleic acids.

15. (original) The method of Claim 14, wherein said primer has a nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, or AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long.

16. (original) The method of Claim 14, wherein an oligonucleotide primer comprising nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID.

NO.:1) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.

17. (original) The method of Claim 14, wherein an oligonucleotide primer comprising nucleotide sequence AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.

18. (original) The method of Claim 14, wherein said oligonucleotide primer is labeled with a fluorescent dye.

19. (original) The method of Claim 18, wherein said dye is SYBR Green I, YO-PRO-1, thiazole orange, Hex, FAM or TET.